

1

SEQUENCE LISTING

<110> SunGene GmbH & Co KGaA

<120> A process for preparing zeaxanthin and/or biosynthetic intermediates and/or secondary products thereof

<130> NAE 439/02

<160> 43

<170> PatentIn version 3.1

<210> 1

<211> 777

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> promoter

<222> (1)..(777)

<223>

<400> 1

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ccaaacatta tctacaaaca aagacttttc tcttaacttg tgattccttc ttaaacccta      240
ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta      300
atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca      360
tatatatctc tttcttctta tttcccaa ataacagacaa aagtagaata ttggctttta      420
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca      480
aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtogatgt      540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta      600
tcacttagtt ttcatcaact tctgaactta cttttcatgg attaggcaat actttccatt      660
tttagtaact caagtggaacc ctttacttct tcaactccat ctctctcttt ctatttcact      720
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 <222> (1)..(212)
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 aaatttgttg atgtgcaggt atcaccggat cc 212

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 <213> Tagetes erecta

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 <222> (141)..(1691)
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 agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
 Met Ser Met Arg Ala Gly His Met Thr Ala Thr
 1 5 10

3

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|---|-----|
| atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg | 221 |
| Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr | |
| 15 20 25 | |
| aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa | 269 |
| Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln | |
| 30 35 40 | |
| gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tgc gag ctg | 317 |
| Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu | |
| 45 50 55 | |
| ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc | 365 |
| Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser | |
| 60 65 70 75 | |
| cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt | 413 |
| Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser | |
| 80 85 90 | |
| aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt | 461 |
| Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu | |
| 95 100 105 | |
| gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc | 509 |
| Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile | |
| 110 115 120 | |
| ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa | 557 |
| Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu | |
| 125 130 135 | |
| ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat | 605 |
| Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp | |
| 140 145 150 155 | |
| act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc | 653 |
| Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala | |
| 160 165 170 | |
| tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg | 701 |
| Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg | |
| 175 180 185 | |
| tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att | 749 |
| Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile | |
| 190 195 200 | |
| act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc | 797 |
| Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile | |
| 205 210 215 | |
| aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga | 845 |
| Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly | |
| 220 225 230 235 | |
| aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca | 893 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Lys | Leu | Leu | Gln | Tyr | Glu | Leu | Gly | Gly | Pro | Arg | Val | Cys | Val | Gln | Thr | |
| | | | | 240 | | | | | 245 | | | | | 250 | | |
| gct | tat | ggt | ata | gag | gtt | gag | gtt | gaa | agc | ata | ccc | tat | gat | cca | agc | 941 |
| Ala | Tyr | Gly | Ile | Glu | Val | Glu | Val | Glu | Ser | Ile | Pro | Tyr | Asp | Pro | Ser | |
| | | | 255 | | | | | 260 | | | | | 265 | | | |
| cta | atg | gtt | ttc | atg | gat | tat | aga | gac | tac | acc | aaa | cat | aaa | tct | caa | 989 |
| Leu | Met | Val | Phe | Met | Asp | Tyr | Arg | Asp | Tyr | Thr | Lys | His | Lys | Ser | Gln | |
| | | 270 | | | | | 275 | | | | | 280 | | | | |
| tca | cta | gaa | gca | caa | tat | cca | aca | ttt | ttg | tat | gtc | atg | cca | atg | tct | 1037 |
| Ser | Leu | Glu | Ala | Gln | Tyr | Pro | Thr | Phe | Leu | Tyr | Val | Met | Pro | Met | Ser | |
| | 285 | | | | | 290 | | | | | 295 | | | | | |
| cca | act | aaa | gta | ttc | ttt | gag | gaa | act | tgt | ttg | gct | tca | aaa | gag | gcc | 1085 |
| Pro | Thr | Lys | Val | Phe | Phe | Glu | Glu | Thr | Cys | Leu | Ala | Ser | Lys | Glu | Ala | |
| 300 | | | | 305 | | | | | 310 | | | | | 315 | | |
| atg | cct | ttt | gag | tta | ttg | aag | aca | aaa | ctc | atg | tca | aga | tta | aag | act | 1133 |
| Met | Pro | Phe | Glu | Leu | Leu | Lys | Thr | Lys | Leu | Met | Ser | Arg | Leu | Lys | Thr | |
| | | | 320 | | | | | 325 | | | | | 330 | | | |
| atg | ggg | atc | cga | ata | acc | aaa | act | tat | gaa | gag | gaa | tgg | tca | tat | att | 1181 |
| Met | Gly | Ile | Arg | Ile | Thr | Lys | Thr | Tyr | Glu | Glu | Glu | Trp | Ser | Tyr | Ile | |
| | | | 335 | | | | | 340 | | | | 345 | | | | |
| cca | gta | ggt | gga | tcc | tta | cca | aat | acc | gag | caa | aag | aac | ctt | gca | ttt | 1229 |
| Pro | Val | Gly | Gly | Ser | Leu | Pro | Asn | Thr | Glu | Gln | Lys | Asn | Leu | Ala | Phe | |
| | | 350 | | | | | 355 | | | | | 360 | | | | |
| ggt | gct | gct | gct | agc | atg | gtg | cat | cca | gcc | aca | gga | tat | tcg | gtt | gta | 1277 |
| Gly | Ala | Ala | Ala | Ser | Met | Val | His | Pro | Ala | Thr | Gly | Tyr | Ser | Val | Val | |
| | 365 | | | | | 370 | | | | | 375 | | | | | |
| aga | tca | ctg | tca | gaa | gct | cct | aat | tat | gca | gca | gta | att | gca | aag | att | 1325 |
| Arg | Ser | Leu | Ser | Glu | Ala | Pro | Asn | Tyr | Ala | Ala | Val | Ile | Ala | Lys | Ile | |
| 380 | | | | 385 | | | | | 390 | | | | | | 395 | |
| tta | ggg | aaa | gga | aat | tca | aaa | cag | atg | ctt | gat | cat | gga | aga | tac | aca | 1373 |
| Leu | Gly | Lys | Gly | Asn | Ser | Lys | Gln | Met | Leu | Asp | His | Gly | Arg | Tyr | Thr | |
| | | | 400 | | | | | 405 | | | | | 410 | | | |
| acc | aac | atc | tca | aag | caa | gct | tgg | gaa | aca | ctt | tgg | ccc | ctt | gaa | agg | 1421 |
| Thr | Asn | Ile | Ser | Lys | Gln | Ala | Trp | Glu | Thr | Leu | Trp | Pro | Leu | Glu | Arg | |
| | | | 415 | | | | | 420 | | | | 425 | | | | |
| aaa | aga | cag | aga | gca | ttc | ttt | ctc | ttt | gga | tta | gca | ctg | att | gtc | cag | 1469 |
| Lys | Arg | Gln | Arg | Ala | Phe | Phe | Leu | Phe | Gly | Leu | Ala | Leu | Ile | Val | Gln | |
| | | 430 | | | | | 435 | | | | | 440 | | | | |
| atg | gat | att | gag | ggg | acc | cgc | aca | ttc | ttc | cgg | act | ttc | ttc | cgc | ttg | 1517 |
| Met | Asp | Ile | Glu | Gly | Thr | Arg | Thr | Phe | Phe | Arg | Thr | Phe | Phe | Arg | Leu | |
| | 445 | | | | | 450 | | | | 455 | | | | | | |
| ccc | aca | tgg | atg | tgg | tgg | ggg | ttt | ctt | gga | tct | tcg | tta | tca | tca | act | 1565 |
| Pro | Thr | Trp | Met | Trp | Trp | Gly | Phe | Leu | Gly | Ser | Ser | Leu | Ser | Ser | Thr | |

460 465 470 475
 gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc 1613
 Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser
 480 485 490
 ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga 1661
 Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly
 495 500 505
 aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag 1711
 Thr Met Leu Lys Ala Tyr Leu Thr Ile
 510 515
 tttagattat aggcacatct tgcatatata tatgtataaa ccttatgtgt gctgtatcct 1771
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<400> 5

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Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
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Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
 35 40 45

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
 115 120 125

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
 130 135 140

Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu
 145 150 155 160

Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser
 165 170 175

Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly
 180 185 190

Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn
 195 200 205

Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg
 210 215 220

Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr
 225 230 235 240

Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu
 245 250 255

Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met
 260 265 270

Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln
 275 280 285

Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe
 290 295 300

Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu
 305 310 315 320

Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile
 325 330 335

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350

7

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
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Met Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380

Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn
 385 390 395 400

Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415

Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445

Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460

Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480

Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
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Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
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Tyr Leu Thr Ile
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gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180
ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240
caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300
gaaagccggg ggatcggagc tgctttttgt tcaaatagcaa cagaataagt ccatggatgc 360
acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420
ctgtatactg gatttggttg tcgac 445

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<223>

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gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180
ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240
caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300
gaaagccggg ggatcggagc tgctttttgt tcaaatagcaa cagaataagt ccatggatgc 360
acagtctagc ctatcccaaa agctcccaag ggtaccaata ggaggaggag gagacagtaa 420
ctgtatactg gatttggttg gaccc 446

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<210> 8
<211> 393
<212> DNA
<213> Tagetes erecta

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<222> (1)..(393)
<223>

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```

<400> 8

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gacttttcttc cgcttgccca catggatgtg gtggggggtt cttggatctt cgttatcatc      120
aactgacttg ataatatattg cgttttacat gtttatcata gcaccgcata gcctgagaat      180
gggtctgggtt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct      240
cacgatataa ataactctag tcgcgatcag tttagattat aggcacatct tgcatatata      300
tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct      360
tggggtaatg ctgatgaagt attttctgtc gac                                     393

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<210> 9
<211> 397
<212> DNA
<213> Tagetes erecta

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<220>
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<222> (1)..(397)
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tccggacttt cttccgcttg cccacatgga tgtgggtgggg gtttcttgga tcttcgttat      120
catcaactga cttgataata tttgcgtttt acatgtttat catagcaccg catagcctga      180
gaatgggtct ggttagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt      240
atctcacgat ataaataact ctagtcgcga tcagtttaga ttataggcac atcttgcata      300
tatatatgta taaaccttat gtgtgctgta tccttacatc aacacagtca ttaattgtat      360
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<210> 10
<211> 1537
<212> DNA
<213> -

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<222> (1)..(1537)
<223>

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| | |
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| tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt | 180 |
| tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaattgtcc | 240 |
| caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt | 300 |
| aatacaaata aagtgaaaca aaatatctat aaataaaca atatatatat tttgttagac | 360 |
| gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg | 420 |
| tttctcatat ttacctttta acccccacaa aaaaaatta taaaaaagaa agaaaaagc | 480 |
| taaaccctat ttaaataagct aactataaga tcttaaaatt atcctcatca gtgtatagtt | 540 |
| taattgggta ttaacttata acattatata tctatgacat atactctctc ctagctattt | 600 |
| ctcacatttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat | 660 |
| gctctaattt gattaacaaa aagttagaaa tattttattta aataaaaaag actaataaat | 720 |
| atataaaatg aatgttcata cgcagacca tttagagatg agtatgcttt cacatgctga | 780 |
| gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca | 840 |
| aaattaacct gctcgtggtt gctgtatatg ggaggctaca aaataaatta aactaaagat | 900 |
| gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg | 960 |
| cacaacccaa ttctattttc gttccttggt ggctggggtt ctcaacagg tcaatagtca | 1020 |
| atattagggt ttattggact tttaatagta tcaaacaaat ctatgtgtga acttaaaaat | 1080 |
| tgtattaaat atttagggta acctgttgcc gtttttagaa taatgtttct tcttaataca | 1140 |
| cgaaagcgta ttgtgtattc attcatttgg cgctcacat gcttcgggtg gctcgttta | 1200 |
| gtctctgcct tctttgtata ttgtactccc cctcttccta tgccacgtgt tctgagctta | 1260 |
| acaagccacg ttgcgtgcc a ttgccaaaca agtcatttta acttcacaag gtccgatttg | 1320 |
| acctccaaaa caacgacaag tttccgaaca gtcgcaaga tcaagggtat aatcgtcttt | 1380 |
| ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt | 1440 |
| taaaacgtag ctgctgttta agtaaatccc agtccttcag tttgtgcttt tgtgtgtttt | 1500 |
| gtttctctga ttacggaat ttggaaataa taagctt | 1537 |

<210> 11
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 <212> DNA
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<220>
 <221> variation

<222> (1)..(734)
 <223>

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 cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cgggtggatcg 180
 gagctgcttt ttgttcaa at gcaacagaat aagtccatgg atgcacagtc tagcctatcc 240
 caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300
 gatatttaga tagattagct atcacctgtg ctgtgggtgtg cagctcccaa gggctcttacc 360
 gatagtaaaa tcgttagtta tgattaatac ttgggagggtg ggggattata ggctttgttg 420
 tgagaatgtt gagaaagagg ttgacaaat cgggtgtttga atgagggttaa atggagttaa 480
 attaaaataa agagaagaga aagattaaga ggggtgatggg gatattaaag acggscaata 540
 tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600
 tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660
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 acagatacaa ggcg 734

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 <212> DNA
 <213> artificial sequence

<220>
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 <222> (1)..(280)
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 tggcttttaa agatggcttg gctgctaate aactcaacte aactcatatc ctatccattc 180
 aaattcaatt caattctatt gaatgcaaag caaagcaaag caaagggttg ttgttgttgt 240
 tgttgagaga cactccaate caaacagata caaggcgtga 280

<210> 13
 <211> 358

<212> DNA
 <213> *Tagetes erecta*

<220>
 <221> (sense) promotor
 <222> (1)..(358)
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<400> 13
 aagcttaccg atagtaaaat cgtaggttat gattaatact tgggaggtgg gggattatag 60
 gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaa 120
 tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180
 cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240
 aagatggctt ggctgctaact caactcaact caactcatat cctatccatt caaattcaat 300
 tcaattctat tgaatgcaaa gcaaagcaaa gcaaagggtt tttgttggtt ttgtcgac 358

<210> 14
 <211> 361
 <212> DNA
 <213> *Tagetes erecta*

<220>
 <221> (antisense) promotor
 <222> (1)..(361)
 <223>

<400> 14
 ctcgagctta ccgatagtaa aatcgtagt tatgattaat acttgggagg tgggggatta 60
 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt 120
 aaatggagtt taattaaaat aaagagaaga gaaagattaa gagggatgat gggatattaa 180
 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
 taaaagatgg cttggctgct aatcaactca actcaactca tatectatcc attcaaattc 300
 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttgatc 360
 c 361

<210> 15
 <211> 28
 <212> DNA
 <213> artificial sequence

<220>
 <221> Primer

<222> (1)..(28)
<223>

<400> 15
gagctcactc actgatttcc attgcttg

28

<210> 16
<211> 37
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(37)
<223>

<400> 16
cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 17
<211> 34
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(34)
<223>

<400> 17
atcaacggac atcgacttaa cggcgtttgt aaac

34

<210> 18
<211> 25
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(25)
<223>

<400> 18
taagcttttt gttgaagaga tttgg

25

<210> 19
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<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(23)
<223>

<400> 19
gaaaataactt catcagcatt acc

23

<210> 20
<211> 28
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(28)
<223>

<400> 20
gtcgactacg taagtttctg cttctacc

28

<210> 21
<211> 26
<212> DNA
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<220>
<221> Primer
<222> (1)..(26)
<223>

<400> 21
ggatccggtg atacctgcac atcaac

26

<210> 22
<211> 28
<212> DNA
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<220>
<221> Primer
<222> (1)..(28)
<223>

<400> 22
aagcttgcac gaggcaaagc aaaggttg

28

<210> 23

<211> 29
<212> DNA
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<220>
<221> Primer
<222> (1)..(29)
<223>

<400> 23
gtcgacaacc aaatccagta tacagttac

29

<210> 24
<211> 30
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(30)
<223>

<400> 24
aggatccaac caaatccagt atacagttac

30

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<212> DNA
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<220>
<221> Primer
<222> (1)..(28)
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<400> 25
gaattcgac gaggcaaagc aaaggttg

28

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<212> DNA
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<400> 26
aagctttgga ttagcactga ttgtc

25

<210> 27
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<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(29)
<223>

<400> 27
gtcgacagaa aatacttcat cagcattac

29

<210> 28
<211> 29
<212> DNA
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<220>
<221> Primer
<222> (1)..(29)
<223>

<400> 28
ggatccagaa aatacttcat cagcattac

29

<210> 29
<211> 27
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(27)
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<400> 29
gaattctctt tggattagca ctgattg

27

<210> 30
<211> 23
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(23)
<223>

<400> 30
cgcccttgat ctgtttggat tgg 23

<210> 31
<211> 24
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(24)
<223>

<400> 31
ctaacaatca atgagtatga gagc 24

<210> 32
<211> 26
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(26)
<223>

<400> 32
agagcaaggc cagcaggacc acaacc 26

<210> 33
<211> 26
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(26)
<223>

<400> 33
ccttgggagc ttttgggata ggctag 26

<210> 34
<211> 26
<212> DNA
<213> artificial sequence

<220>
<221> Primer

<222> (1)..(26)
<223>

<400> 34
tcacgccttg tatctgtttg gattgg

26

<210> 35
<211> 15
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(15)
<223>

<400> 35
gtcgagtatg gagtt

15

<210> 36
<211> 28
<212> DNA
<213> artificial sequence

<220>
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<223>

<400> 36
aagcttaccg atagtaaaat cgttagtt

28

<210> 37
<211> 31
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(31)
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<400> 37
ctcgagctta ccgatagtaa aatcgttagt t

31

<210> 38
<211> 28
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(28)
<223>

<400> 38
gtcgacaaca acaacaaaca acctttgc

28

<210> 39
<211> 28
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(28)
<223>

<400> 39
ggatccaaca acaacaaaca acctttgc

28

<210> 40
<211> 28
<212> DNA
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<220>
<221> Primer
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<223>

<400> 40
gtcgactttt tgttgaagag atttggtg

28

<210> 41
<211> 28
<212> DNA
<213> artificial sequence

<220>
<221> Primer
<222> (1)..(28)
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<400> 41
ctcgagactc actgatttcc attgcttg

28

<210> 42

<211> 22
 <212> DNA
 <213> artificial sequence

<220>
 <221> Primer
 <222> (1)..(22)
 <223>

<400> 42
 gagctctaca aattagggtt ac

22

<210> 43
 <211> 23
 <212> DNA
 <213> artificial sequence

<220>
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 <222> (1)..(23)
 <223>

<400> 43
 aagcttatta tttccaaatt ccg

23